

FIGURE 1

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GCTCCCAGCCAAGAACCTCGGGGCGCTGCGCGGTGGGGAGGAGTTCCCCGAAACCCGGCCG
CTAAGCGAGGCCTCCTCCTCCCGCAGATCCGAACGGCCTGGGCGGGGTACCCCGGCTGGGA
CAAGAAGCCGCCGCTGCCTGCCCCGGGCGGGGAGGGGGCTGGGGCTGGGGCCGGAGGCGG
GGTGTGAGTGGGTGTGTGCGGGGGGCGGAGGCTTGATGCAATCCCGATAAGAAATGCTCGGG
TGTCTTGGGCACCTACCCGTGGGGCCCGTAAGGCGCTACTATATAAGGCTGCCGGCCGGAG
CCGCCGCGCCGTGAGAGCAGGAGCGCTGCGTCCAGGATCTAGGGCCACGACCATCCCAACCC
GGCACTCACAGCCCCGAGCGCATCCCGGTGCGCGCCAGCCTCCCGCACCCTCATCGCCGG
AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGTGGTGGTCCACGTATGG
ATCCTGGCCGGCCTCTGGCTGGCCGTGGCCGGGCGCCCCCTCGCCTTCTCGGACGCGGGGCC
CCACGTGCACTACGGCTGGGGCGACCCCATCCGCCTGCGGCACCTGTACACCTCCGGCCCCC
ACGGGCTCTCCAGCTGCTTCTGCGCATCCGTGCCGACGGCGTCTGCGGACCGTGGCCATCAAGGG
CAGAGCGCGCACAGTTTGTGGAGATCAAGGCAGTCGCTCTGCGGACCGTGGCCATCAAGGG
CGTGACAGCGTGCGGTACCTCTGCATGGGCGCCGACGGCAAGATGCAGGGGCTGCTTCAGT
ACTCGGAGGAAGACTGTGCTTTCGAGGAGGAGATCCGCCAGATGGCTACAATGTGTACCGA
TCCGAGAAGCACCGCCTCCCGGTCTCCCTGAGCAGTGCCAAACAGCGGCAGCTGTACAAGAA
CAGAGGCTTTCTTCCACTCTCTCATTTCTGCCCCATGCTGCCCCATGGTCCCAGAGGAGCCTG
AGGACCTCAGGGGGCACTTGGAACTGTGACATGTTCTCTTCGCCCCCTGGAGACCGACAGCATG
GACCCATTTGGGCTTGTACCCGACTGGAGGCGGTGAGGAGTCCCAGCTTTGAGAAGTAACCT
GAGACCATGCCCCGGGCTTCTACTGCTGCCAGGGGCTGTGGTACCTGCAGCGTGGGGGACG
TGCTTCTACAAGAACAGTCCTGAGTCCACGTTCTGTTTAGCTTTAGGAAGAAACATCTAGAA
GTTGTACATATTCAGAGTTTTCCATTGGCAGTGCCAGTTTCTAGCCAATAGACTTGTCTGAT
CATAACATTGTAAGCCTGTAGCTTGCCAGCTGCTGCCTGGGCCCCCATTCTGCTCCCTCGA
GGTTGCTGGACAAGCTGCTGCACTGTCTCAGTTCTGCTTGAATACCTCCATCGATGGGGAAC
TCACTTCCTTTGGAAAAATTCTTATGTCAAGCTGAAATTCTCTAATTTTTTCTCATCACTTC
CCCAGGAGCAGCCAGAAGACAGGCAGTAGTTTTAATTTACAGGAACAGGTGATCCACTCTGTA
AAACAGCAGGTAAATTTCACTCAACCCCATGTGGGAATTGATCTATATCTCTACTTCCAGGG
ACCATTTGCCCTTCCCAAATCCCTCCAGGCCAGAACTGACTGGAGCAGGCATGGCCACCAG
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAACCTGAGAATTCCCC
CTGAGGCCAGTTCTGTCATGGATGCTGTCCTGAGAATAACTTGCTGTCCCGGTGTCACCTGC
TTCCATCTCCCAGCCCACCAGCCCTCTGCCACCTCACATGCCTCCCCATGGATTGGGGCCT
CCCAGGCCCCCACCTTATGTCAACCTGCACTTCTTGTTCAAAAATCAGGAAAAGAAAAGAT
TTGAAGACCCCAAGTCTTGTCAATAACTTGCTGTGTGGAAGCAGCGGGGGAAGACCTAGAAC
CCTTTCCCCAGCACTTGGTTTTTCCAACATGATATTTATGAGTAATTTATTTTGATATGTACA
TCTCTTATTTTCTTACATTATTTATGCCCCCAAATATATTTATGTATGTAAGTGAGGTTTG
TTTTGTATATTAAAATGGAGTTTGTGTG

FIGURE 2

MRSGCVVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWDPIRLRHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSILLEIKAVALRTVAIKGVHVSRYLCMGADGKMQLLYSEEDCAFEE
EIRPDGYNVYRSEKHRLPVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD
MFSSPLETDSMDPFGLVTGLEAVRSPSEK

signal peptide:
amino acids 1-22

N-myristoylation sites:
amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site:
amino acids 48-59

HBGF/FGF domain:
amino acids 80-131

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FIGURE 3A

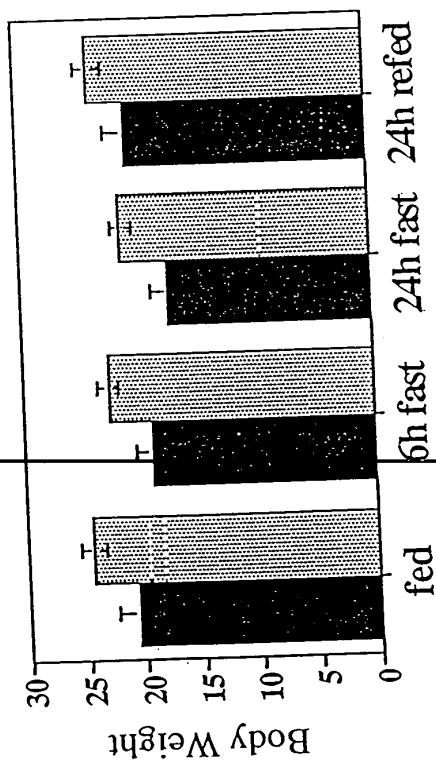


FIGURE 3B

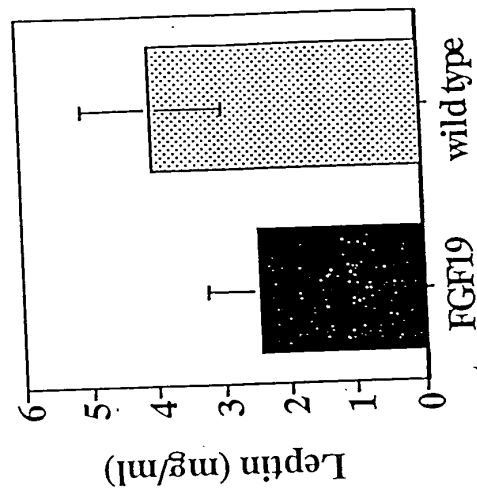


FIGURE 4A

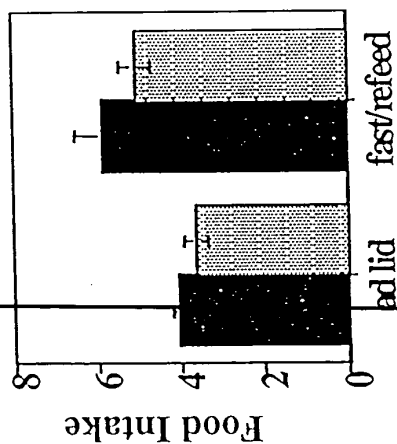


FIGURE 4B

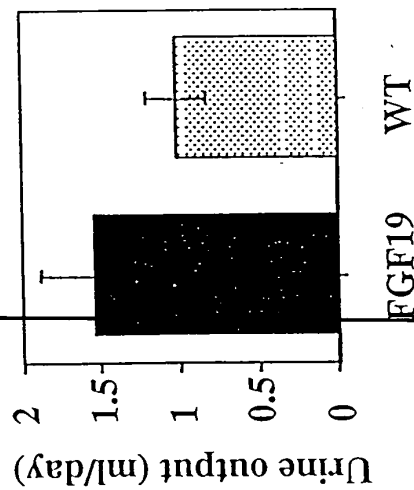
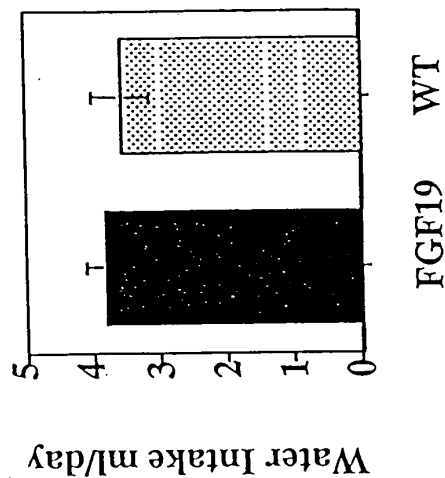


FIGURE 4C

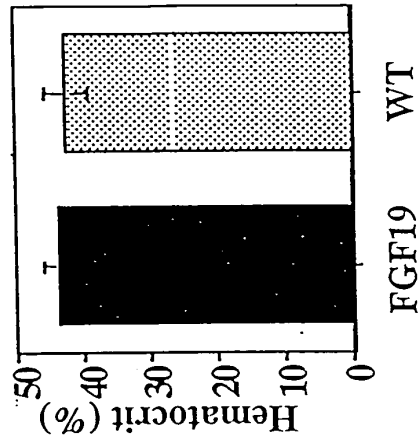


FIGURE 4D

FIGURE 5

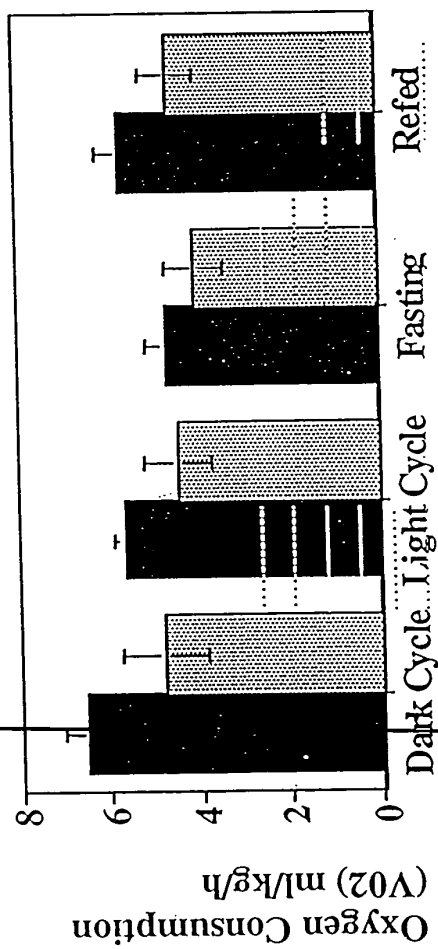


FIGURE 6B

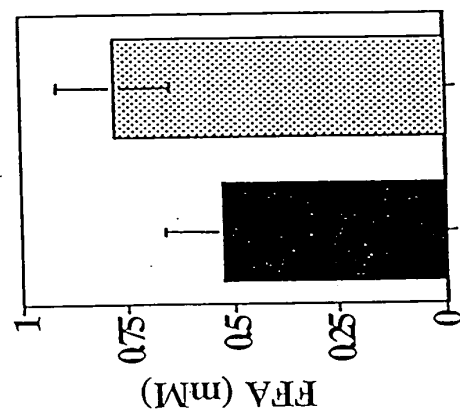


FIGURE 6A

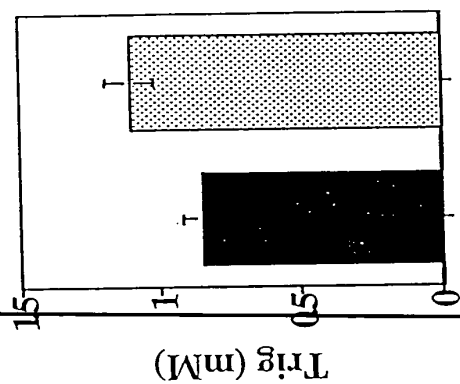


FIGURE 7B

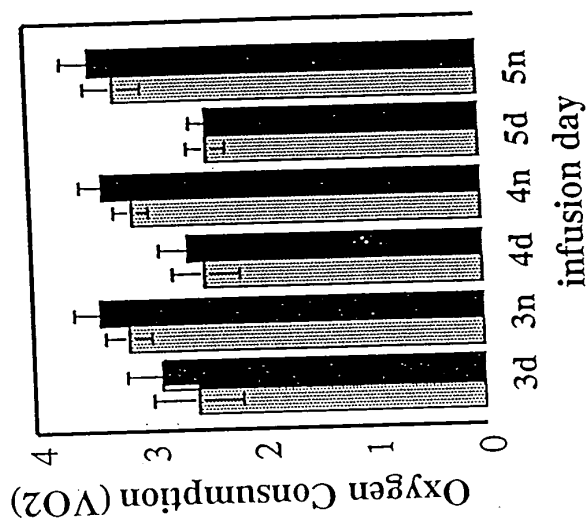
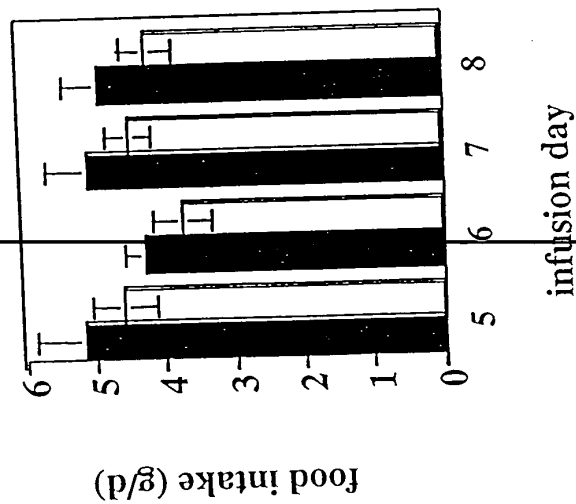


FIGURE 7A



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FIGURE 8A

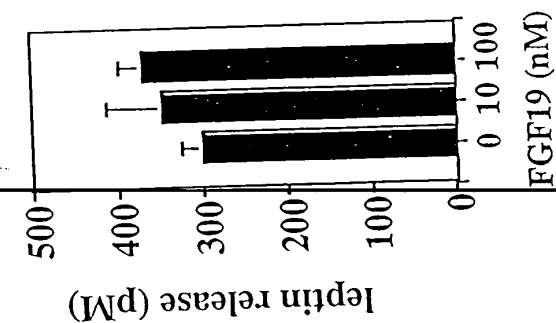
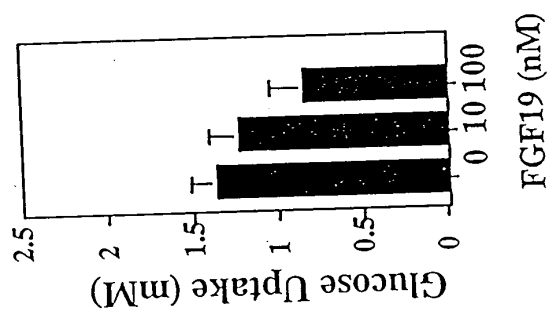


FIGURE 8B



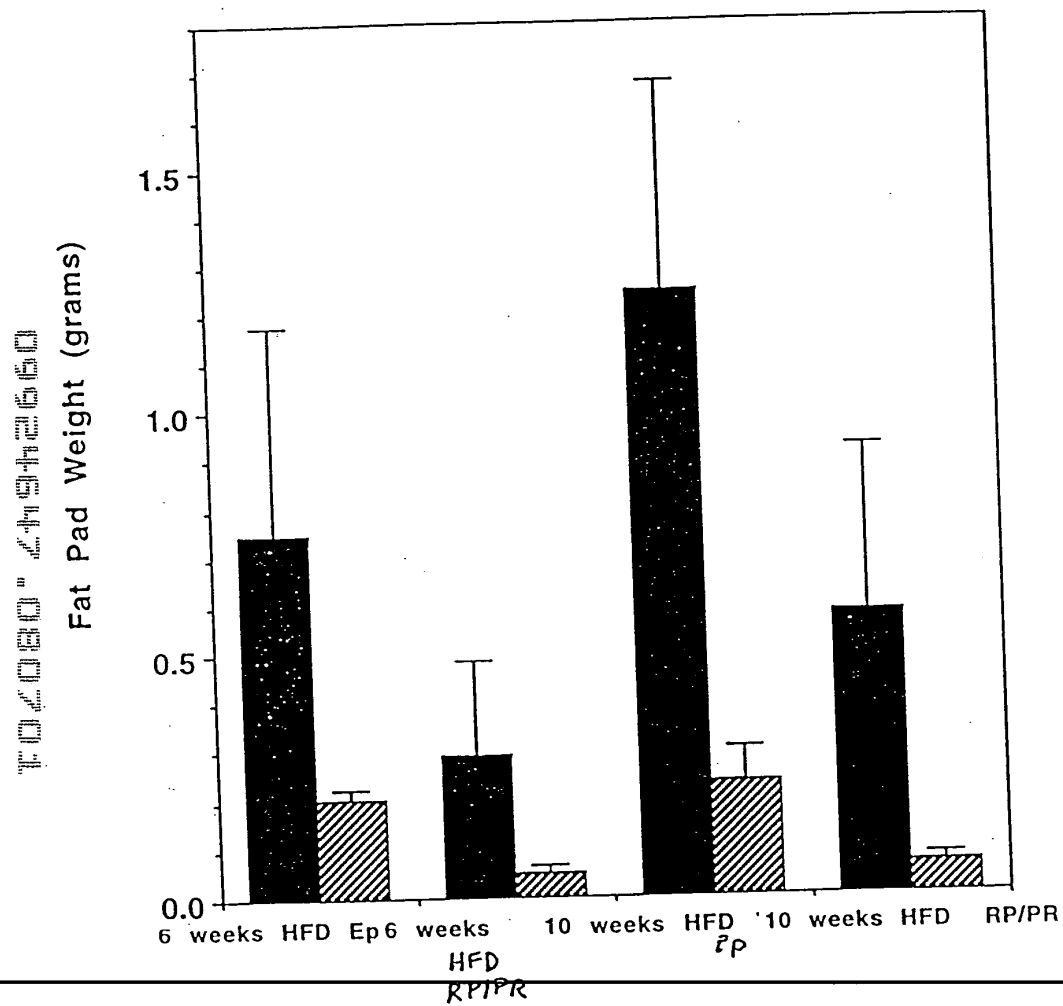


FIGURE 9

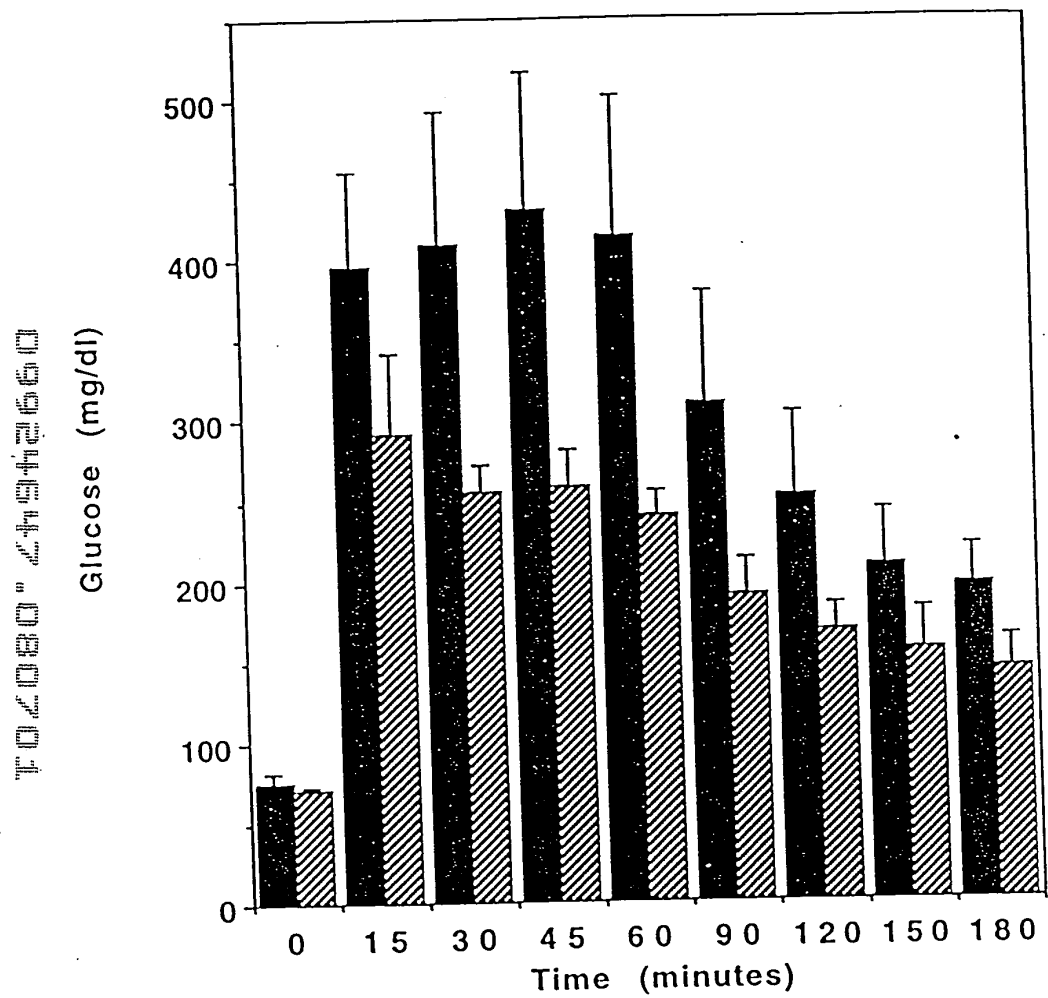


FIGURE 10

Fig. 11

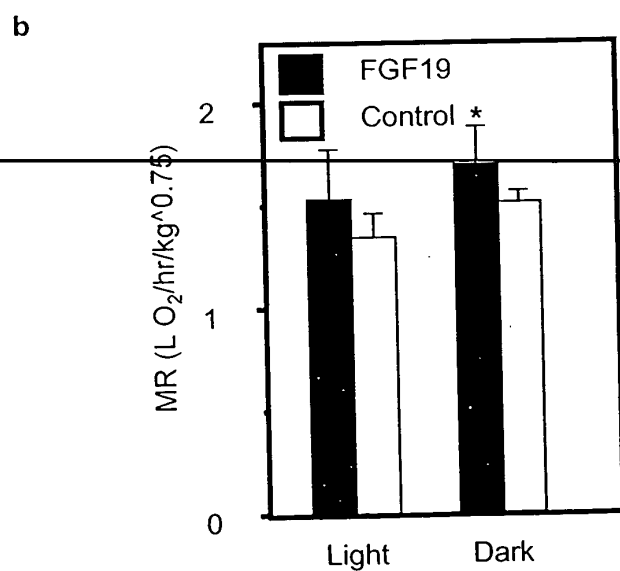
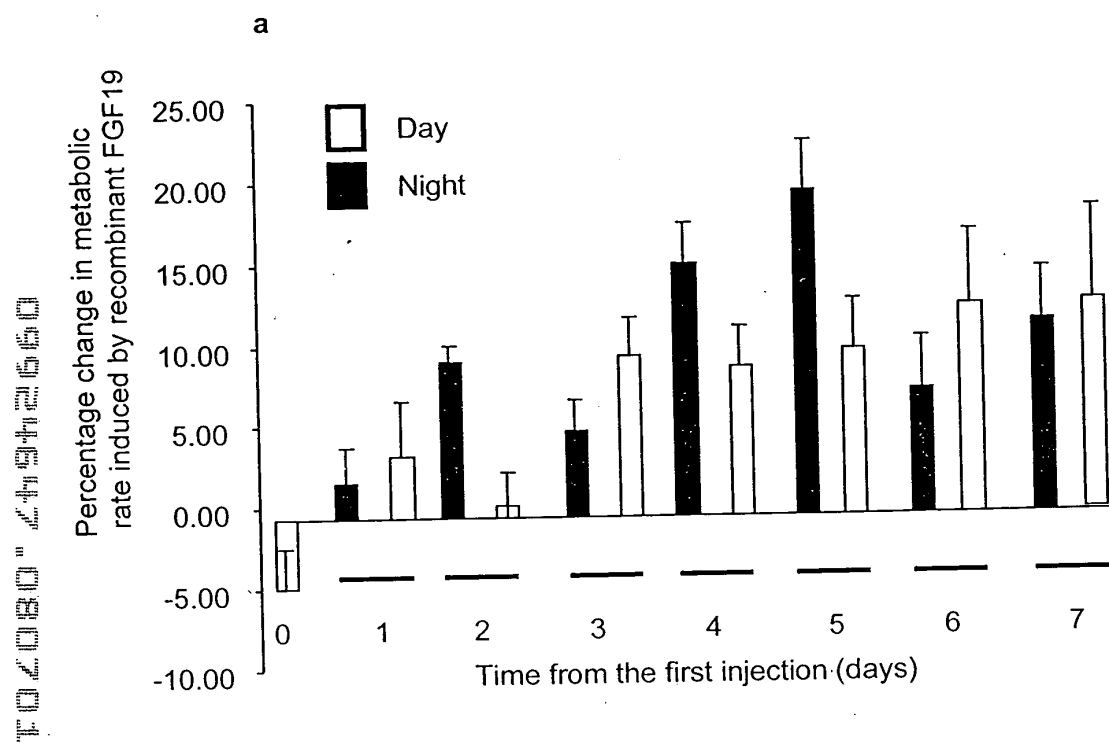


Fig 12

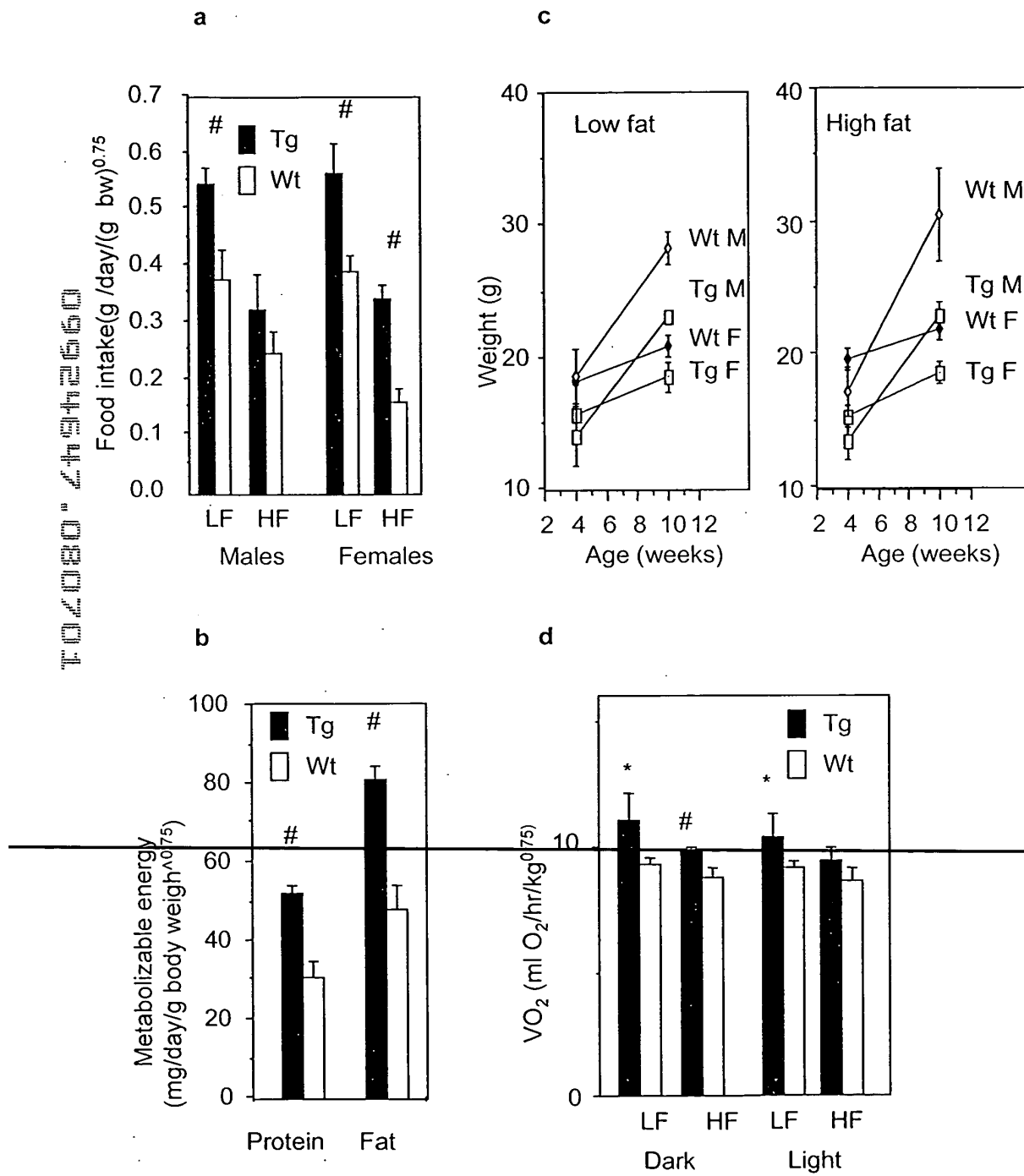


Fig. 13

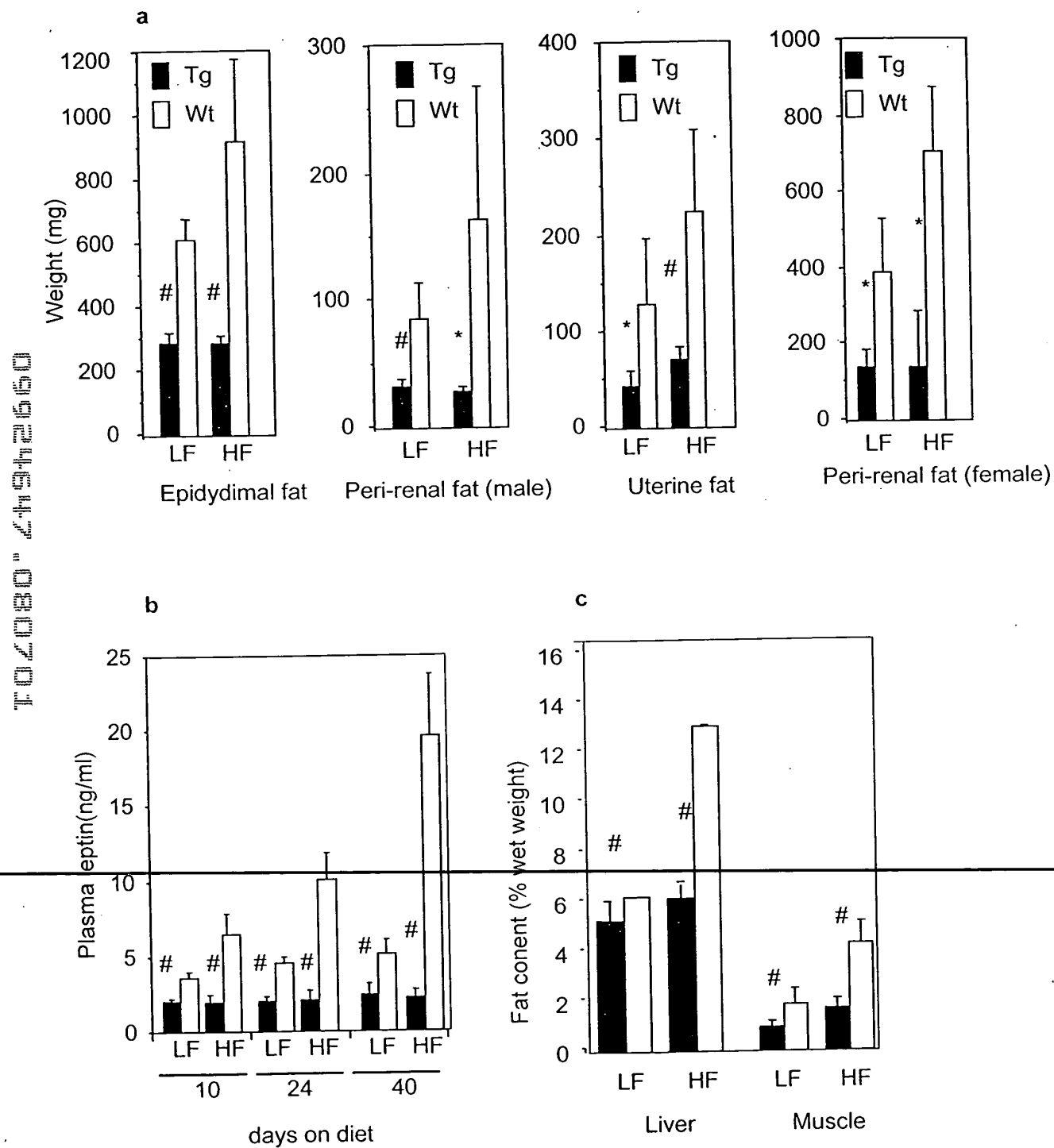


Fig. 14.

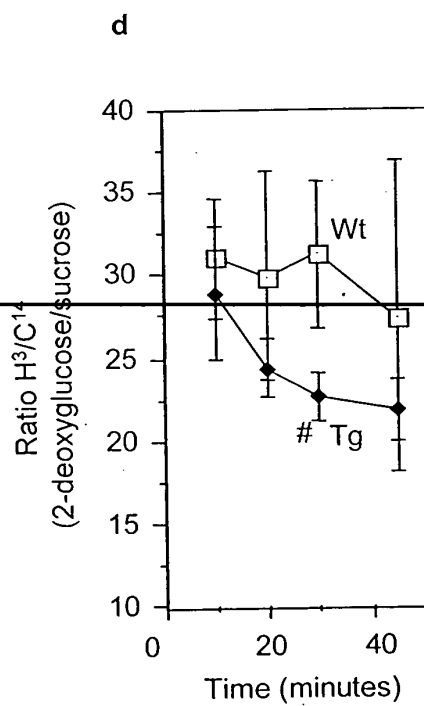
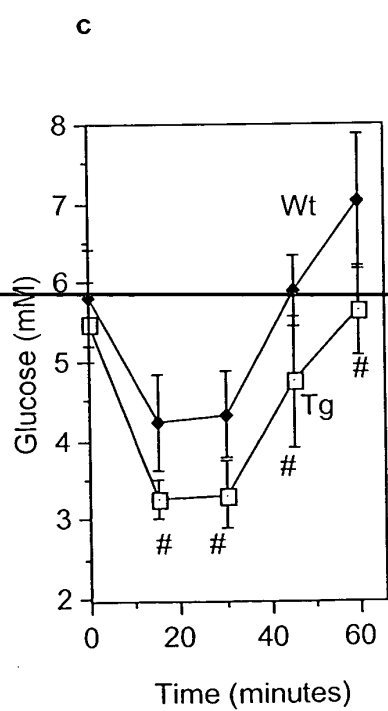
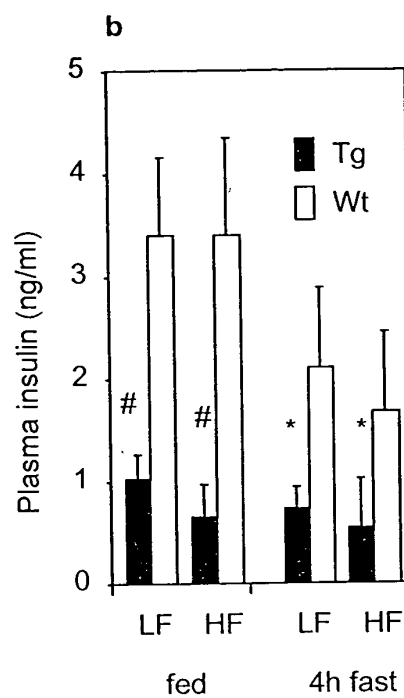
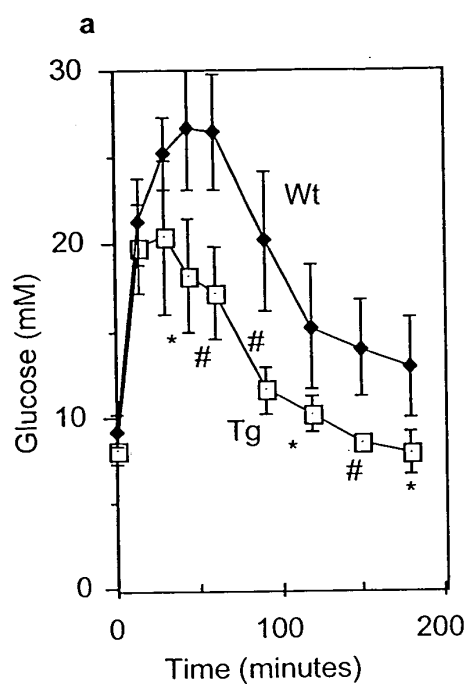


Fig. 15.

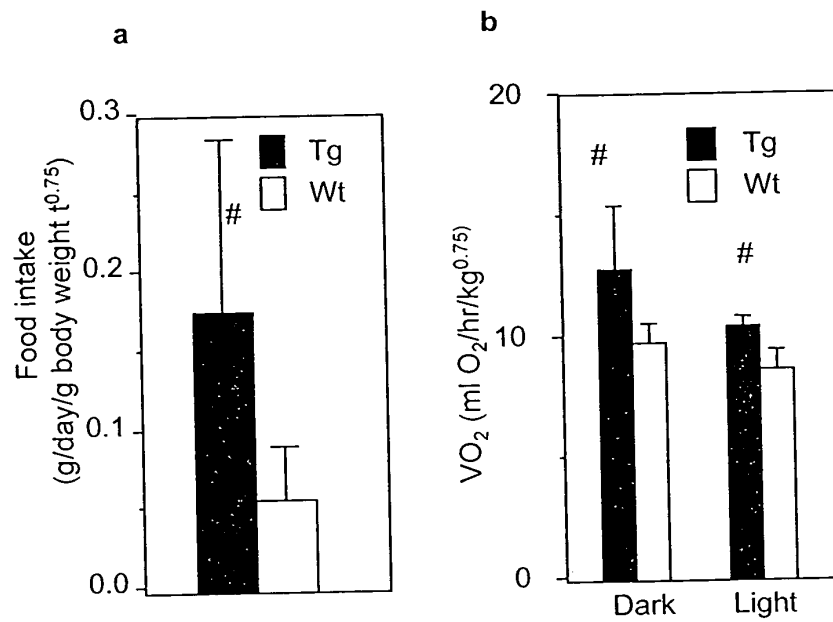


Figure 16

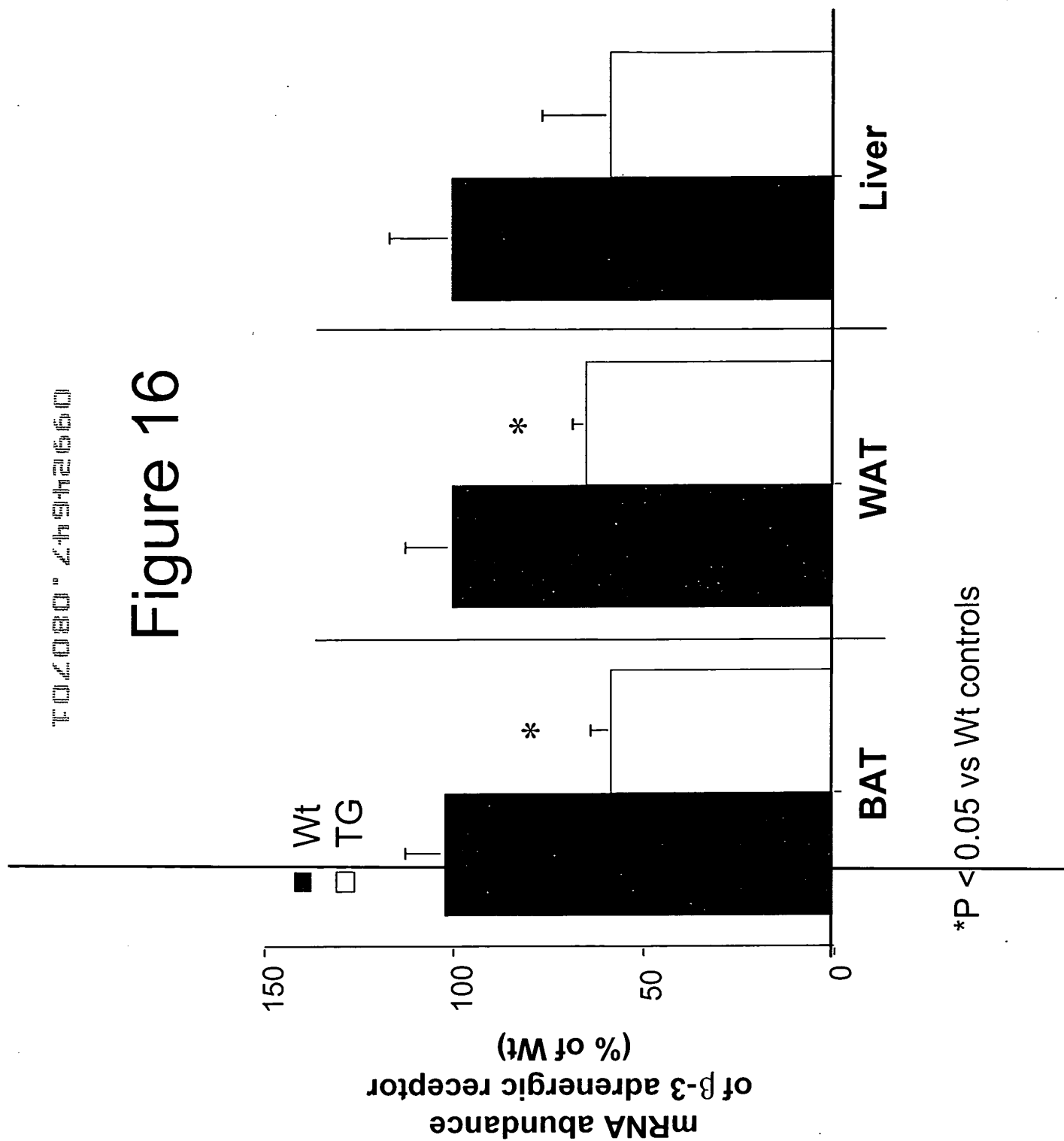
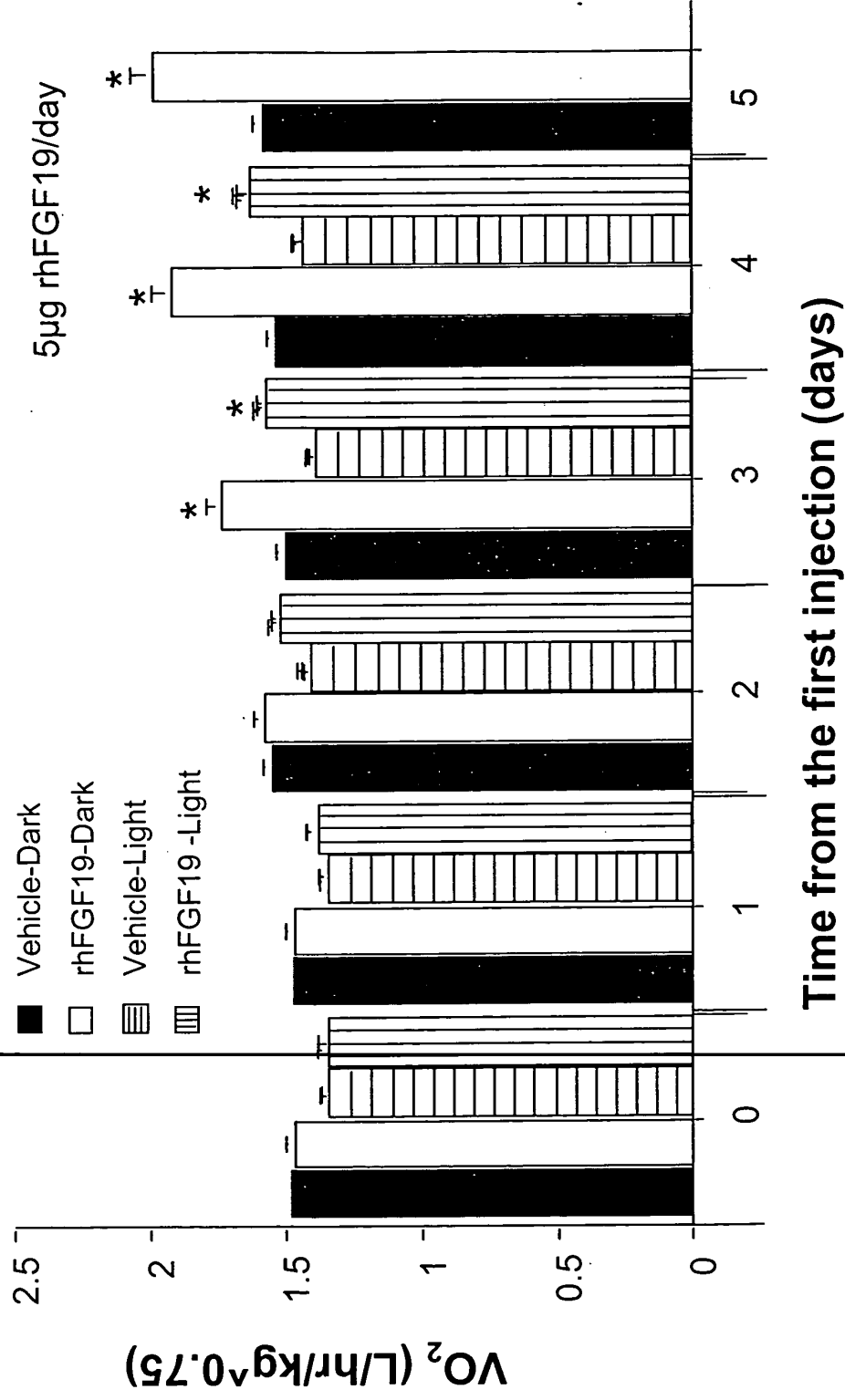


Figure 17



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Figure 18

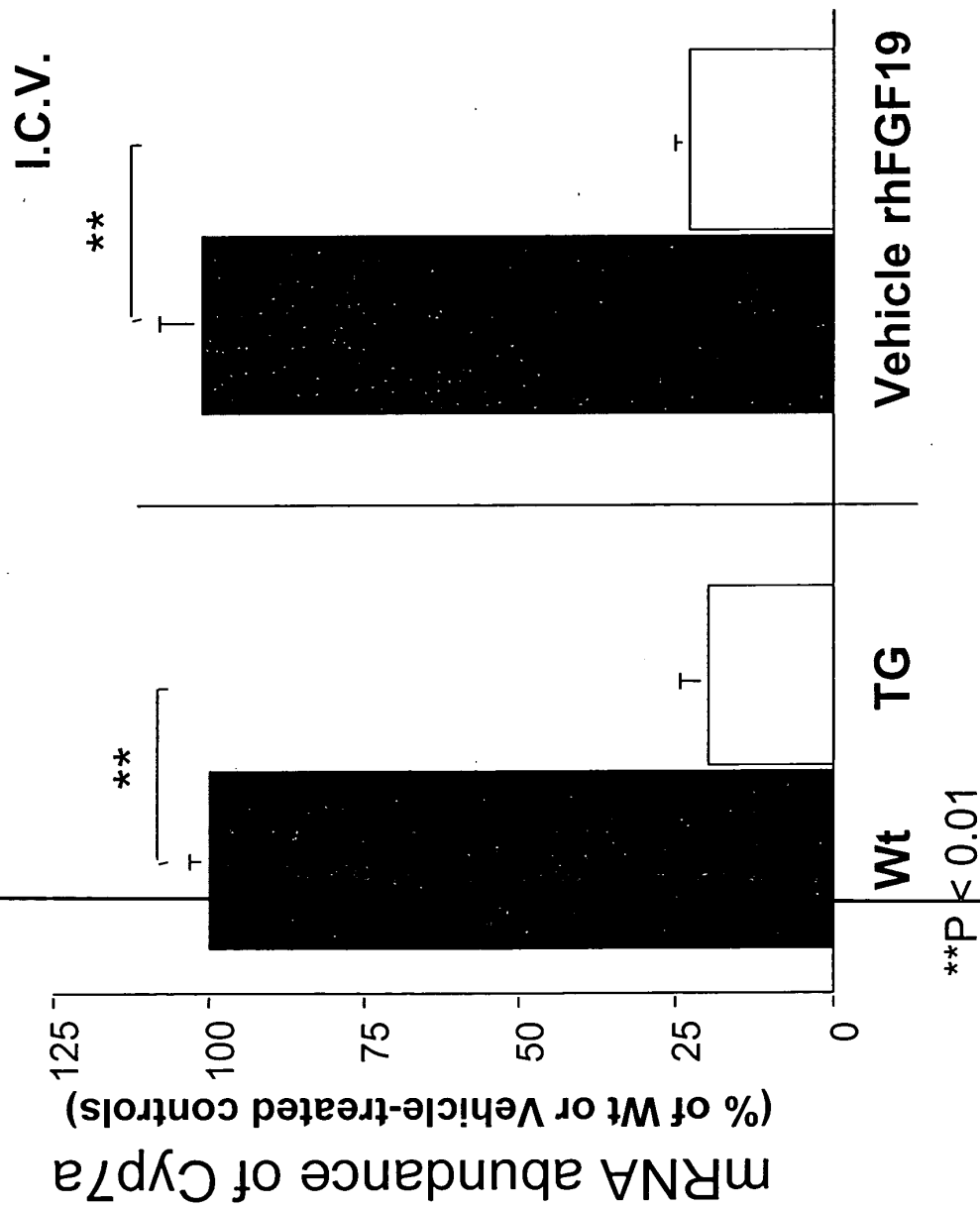


Figure 19

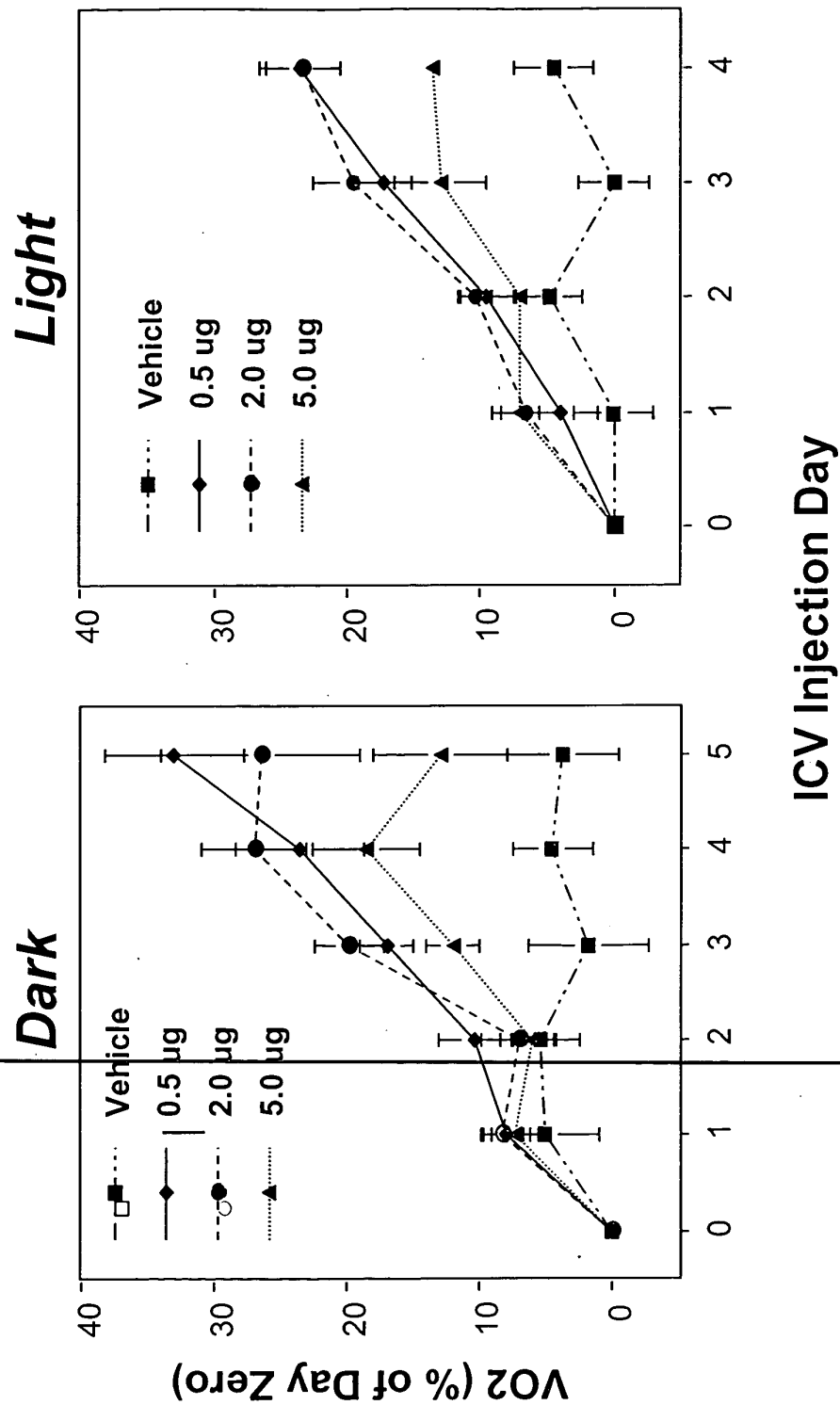


Figure 20

	Vehicle	rhFGF19		
		5.0 µg	2.0 µg	0.5 µg
NPY	1.0 +/- 0.08	0.81 +/- 0.23	0.63 +/- 0.20	0.40 +/- 0.08
AgRP	1.0 +/- 0.33	0.26 +/- 0.10	0.57 +/- 0.26	0.29 +/- 0.16
POMC	1.0 +/- 0.27	1.49 +/- 0.42	3.48 +/- 1.5	38.77 +/- 3.32
MC4-R	1.0 +/- 0.16	0.47 +/- 0.09	0.70 +/- 0.10	0.48 +/- 0.08

